

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

M protein - protein search, using sw model

Run on: March 15, 2006, 13:39:12 ; Search time 164 Seconds
(without alignments)
135.030 Million cell updates/sec

Title: US-10-820-640A-2
Perfect score: 317
Sequence: 1 NSDSCGCPSPHDGYCLNGVC.....VINGNRCQTRDLKWEELR 53

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	317	100.0	53	5	
2	270	85.2	112	4	
3	270	85.2	112	4	
4	264	83.3	53	4	
5	264	83.3	53	4	
6	264	83.3	53	4	
7	264	83.3	145	4	
8	264	83.3	1214	4	
9	262	82.6	53	3	
10	262	82.6	53	3	
11	262	82.6	53	4	
12	262	82.6	53	4	
13	262	82.6	53	4	
14	262	82.6	53	4	
15	262	82.6	53	4	
16	262	82.6	53	4	
17	262	82.6	53	4	
18	262	82.6	53	5	
19	262	82.6	53	5	
20	262	82.6	53	5	
21	262	82.6	53	5	
22	262	82.6	53	5	
23	262	82.6	53	5	
24	262	82.6	53	5	
25	262	82.6	53	5	
26	262	82.6	53	5	
27	262	82.6	53	5	

28	262	82.6	53	5
29	262	82.6	53	5
30	262	82.6	53	5
31	262	82.6	53	6
32	262	82.6	54	4
33	262	82.6	54	4
34	262	82.6	58	3
35	262	82.6	58	4
36	262	82.6	61	4
37	262	82.6	91	4
38	262	82.6	112	4
39	262	82.6	112	4
40	262	82.6	140	3
41	262	82.6	146	4
42	262	82.6	167	4
43	262	82.6	176	5
44	262	82.6	265	4
45	262	82.6	266	4

ALIGNMENTS

RESULT 1
US-10-820-640A-2
; Sequence 2, Application US/10820640A
; Publication No. US20050032162A1
; GENERAL INFORMATION:
; APPLICANT: Coco, Wayne M.
; APPLICANT: Pienkos, Philip T.
; APPLICANT: Loomis, Katrina A.
; TITLE OF INVENTION: Epidermal Growth Factor Agonists and
; FILE OF INVENTION: Methods of Use
; FILE REFERENCE: 3530.1000 US1
; CURRENT APPLICATION NUMBER: US/10/820,640A
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 60/463,890
; PRIOR FILING DATE: 2003-04-17
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-820-640A-2

Query Match 100.0%; Score 317; DB 5; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.3e-28;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSDSCGCPSPHDGYCLNGVCVMTYALDKYACNCVINGNRCQTRDLKWEELR 53
Db 1 NSDSCGCPSPHDGYCLNGVCVMTYALDKYACNCVINGNRCQTRDLKWEELR 53

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

protein - protein search, using sw model

Run on: March 15, 2006, 13:39:52 ; Search time 23 Seconds
(without alignments)
65.957 Million cell updates/sec

Title: US-10-820-640A-2

Perfect score: 317

Sequence: 1 NSDSCGCPFDGYCLNGVC.....VIGYNGDRQTRDLKWEIR 53

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB ID	Description
	Score	Match	Length		
1	264	83.3	53	7	
2	262	82.6	53	7	
3	262	82.6	53	7	
4	262	82.6	53	7	
5	262	82.6	53	7	
6	262	82.6	53	7	
7	262	82.6	53	7	
8	262	82.6	53	7	
9	262	82.6	53	7	
10	262	82.6	53	7	
11	262	82.6	53	7	
12	262	82.6	53	7	
13	262	82.6	1207	7	
14	250	78.9	53	7	
15	249	78.5	53	7	
16	215	67.8	46	7	
17	211.5	66.7	52	7	
18	211.5	66.7	52	7	
19	163	51.4	48	7	
20	132	41.6	298	7	
21	108	34.1	330	7	
22	99.5	31.4	154	7	
23	99.5	31.4	159	7	
24	97	30.6	1418	6	
25	95.5	30.1	45	7	

26	95	30.0	1450	6
27	95	30.0	1450	6
28	93.5	29.5	45	7
29	93.5	29.5	50	7
30	93.5	29.5	118	7
31	93.5	29.5	160	6
32	93.5	29.5	169	7
33	93.5	29.5	354	7
34	93.5	29.5	373	7
35	93.5	29.5	380	7
36	93.5	29.5	380	7
37	93.5	29.5	1170	7
38	93.5	29.5	2471	7
39	92.5	29.2	728	7
40	91.5	28.9	380	7
41	91	28.7	1419	7
42	90.5	28.5	152	7
43	88.5	27.9	720	6
44	88.5	27.9	720	7
45	88.5	27.9	720	7

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

M protein - protein search, using sw model

Run on: March 15, 2006, 13:28:47 ; Search time 23 Seconds
(without alignments)
190.514 Million cell updates/sec

Title: US-10-820-640A-2
Perfect score: 317
Sequence: 1 NSDSGCFSDHYCLNGVC.....VIGYNGDRCTRLKWWELR 53

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	264	83.3	53	1	
2	264	83.3	53	2	
3	264	83.3	53	2	
4	262	82.6	53	1	
5	262	82.6	53	1	
6	262	82.6	53	1	
7	262	82.6	53	2	
8	262	82.6	53	2	
9	262	82.6	53	2	
10	262	82.6	53	6	
11	262	82.6	55	6	
12	262	82.6	91	1	
13	262	82.6	91	1	
14	262	82.6	91	1	
15	262	82.6	91	1	
16	262	82.6	91	1	
17	262	82.6	91	1	
18	262	82.6	91	2	
19	262	82.6	91	2	
20	262	82.6	91	4	
21	262	82.6	93	1	
22	262	82.6	93	1	
23	262	82.6	93	2	
24	262	82.6	140	2	
25	262	82.6	176	2	
26	262	82.6	177	2	
27	262	82.6	177	2	

28	262	82.6	181	2
29	262	82.6	181	2
30	262	82.6	186	2
31	262	82.6	239	2
32	262	82.6	293	2
33	262	82.6	293	2
34	262	82.6	293	2
35	262	82.6	293	2
36	262	82.6	293	4
37	262	82.6	293	4
38	262	82.6	309	2
39	262	82.6	332	1
40	257	81.1	53	1
41	257	81.1	53	6
42	251	79.2	53	6
43	244	77.0	48	2
44	244	77.0	88	1
45	242	76.3	51	6